REMARKS

Status of the Claims

Claims 2-4 and 7 were rejected. Claims 1, 5, 6, and 8-24 were withdrawn from consideration due to a restriction requirement and have been canceled without prejudice or disclaimer. Claim 7 has also been canceled without prejudice or disclaimer. Applicants reserve the right to pursue claims 1 and 5-24 in a divisional application. Claims 25-46 have been added. Claims 2-4 and 25-46 are pending.

Amendments to the Claims

Claims 1 and 5-24 have been canceled without prejudice or disclaimer.

Claims 25-46 have been added. Support for these claims can be found throughout the specification and in the originally filed claims.

Specifically, claims 2-4 have been amended to recite a nucleotide sequence having at least "80% sequence identity" to SEQ ID NO:3. Newly added claims 25 and 26 also recite a sequence having at least "80% sequence identity" to SEQ ID NO:3. Support for this amendment can be found, for example, on page 14, lines 23-26 of the specification.

Claims 37-41 have been added and recite the phrase "said stringent conditions comprise hybridization in 50% formamide, 1 M NaCl, and 1% SDS at 37°C and a wash in 0.1x SSC at 60°C to 65°C". Support for this limitation can be found, for example, on page 21, lines 30-31 and page 22, lines 32-33 of the specification.

Claims 42-46 have been added and recite a nucleotide sequence that comprises at least "50" contiguous nucleotides of SEQ ID NO:3. Support for the term "50" contiguous nucleotides can be found, for example, page 14, lines 8-10 of the specification.

Claims 25, 30, 35, 40, and 45 recite "vectors". Support for this term can be found, for example, on pages 44 and 45 of the specification.

No new matter has been added by way of these amendments.

Election/Restriction

The Restriction Requirement mailed June 4, 2002 placed claim 7 in both Group II and III. Applicants elected to pursue Group II and consequently, claims 2-4 and 7 are presently under examination. Applicants have canceled claim 7 without prejudice or disclaimer and reserve the right to purse this claim in a divisional application drawn to the claims encompassed by Group III.

The Objections to the Specification Should Be Withdrawn

The abstract and the title were objected to. The Abstract and title have been amended to recite the elected "LOX sequence". Applicants submit that the abstract and title, as amended, appropriately reflect the claimed invention and the objection should be withdrawn.

The specification has also been amended to recite the address of the ATCC depository and is now in compliance with 37 C.F.R. 1.809.

The Rejection of the Claims Under 35 U.S.C. § 112, First Paragraph, Should Be Withdrawn

Written Description

Claims 2-4 and 7 were rejected under 35 U.S.C. §112, first paragraph, for lack of written description. This rejection is respectfully traversed.

The Examiner asserts the specification "does not describe the composition and structure of other DNA sequences with 60% identity to SEQ ID NO:3, or [sequences] that hybridize under stringent conditions to SEQ ID NO:3 and encode LOX-like polypeptides" (Office Action mailed July 23, 2002, page 3). Applicants respectfully disagree.

Claim 7 has been canceled and new claims 25-46 have been submitted. Applicants will address the Examiner's concern as it applies to claims 2-4 and newly submitted claims 25-46.

Claims 27-31 and 32-36 recite nucleic acid molecules, DNA constructs, cells, and vectors comprising the nucleotide sequence set forth in SEQ ID NO:3, the cDNA insert of the PTA-287 deposit, antisense sequence of SEQ ID NO:3, and the nucleotide sequence encoding the

polypeptide of SEQ ID NO:4. As the specification specifically discloses the sequences recited in these claim, claims 27-31 and 32-36 satisfy the written description requirement of 35 U.S.C. §112, first paragraph.

Claims 2-4 and 25-26 recite nucleic acid molecules, DNA constructs, cells, and vectors comprising a nucleotide sequence having at least 80% sequence identity to the sequence of SEQ ID NO:3, where the nucleotide sequence encodes a polypeptide having LOX-like activity. The Examiner asserts the composition and structure of the other sequences having 60% sequence identity are not provided. This is an improper standard.

The Examiner is reminded that every species encompassed by the claimed invention need not be disclosed in the specification to satisfy the written description requirement of 35 U.S.C. § 112, first paragraph. *Utter v. Hiraga*, 845 F.2d 993, 6 USPQ2d 1709 (Fed. Cir. 1988). In fact, the description of a claimed genus can be by structure, formula, chemical name, or physical properties. See *Ex parte Maizel*, 27 USPQ2d 1662, 1669 (B.P.A.I.1992), *citing Amgen v. Chugai*, 927 F.2d 1200, 1206 (Fed. Cir. 1991).

First, the claims have been amended to recite that the sequence shares 80% sequence identity to the sequence of SEQ ID NO:3. The recitation of at least 80% sequence identity, as recited in claims 2-4 and 25-26, is a *very predictable structure* of the sequences encompassed by the claimed invention. The description of a representative number of species does not require the description to be of such specificity that it would provide individual support for each species that the genus embraces. 66 Fed. Reg. 1099, 1106 (2000). Satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that the Applicants were in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed. 66 Fed. Reg. 1099, 1106 (2000). Applicants submit that the knowledge and level of skill in the art would allow a person of ordinary skill to envision the claimed invention, *i.e.*, a sequence having at least 80% sequence identity to the sequence set forth in SEQ ID NO:3.

Furthermore, the description of a claimed genus can be by structure, formula, chemical name, or physical properties. *See Ex parte Maizel*, 27 USPQ2d 1662, 1669 (B.P.A.I. 1992),

citing Amgen v. Chugai, 927 F.2d 1200, 1206 (Fed. Cir. 1991). A genus of DNAs may therefore be described by means of a recitation of a representative number of DNAs, defined by nucleotide sequence, falling within the scope of the genus, *or* by means of a recitation of structural features common to the genus, which features constitute a substantial portion of the genus. *Regents of the University of California v. Eli Lilly & Co.*, 119 F.3d 1559, 1569 (Fed. Cir. 1997); *see also* Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, first paragraph, "Written Description" Requirement, 66 Fed. Reg. 1099, 1106 (2000). The recitation of a predictable structure of at least 80% sequence identity to SEQ ID NO:3 is sufficient to satisfy the written description requirement.

In addition, an Applicant may rely upon functional characteristics in the description, provided there is a correlation between the function and structure of the claimed invention. *Id.*, *citing Lilly* at 1568. Claims 2-4 and 25-26 recite that the claimed sequences encode a polypeptide having LOX-like activity, thereby providing a functional characterization of the sequences claimed in the genus.

Example 14 of the Revised Interim Written Description Guidelines is directed to a generic claim: a protein having at least 95% sequence identity to the sequence of SEQ ID NO:3, wherein the sequence catalyzes the reaction A → B. The Training Materials concludes that the generic claim of Example 14 is sufficiently described under § 112, first paragraph, because 1) "the single sequence disclosed in SEQ ID NO:3 is representative of the genus" and 2) the claim recites a limitation requiring the compound to catalyze the reaction from A → B. The Guidelines conclude that one of skill in art would recognize that the Applicants were in possession of the necessary common attributes possessed by the members of the genus.

Following the analysis of Example 14, Applicants submit that amended claims 2-4 and 25-26 satisfy the written description requirements of § 112, first paragraph. Specifically, the claims of the present invention encompass sequences having at least 80% sequence identity to the sequence of SEQ ID NO:3, wherein the claimed sequences encode a polypeptide having LOX-like activity. As in Example 14, the specification discloses the nucleic acid sequence of

SEQ ID NO:3, and the amended claims recite a limitation requiring the compound to have a specific function.

Consequently, contrary to the Examiner's conclusion, the sequences encompassed by the genus of claims 2-4 and 25-26 are defined by relevant identifying physical and chemical properties. In fact, the common attributes or features of the elements possessed by the members of the genus is that they encode a polypeptide having LOX-like activity and share at least 80% sequence identity at the nucleotide level to the disclosed nucleotide sequence of SEQ ID NO:3.

Similarly, claims 37-41 recite nucleic acid molecules, DNA constructs, cells, and vectors comprising a nucleotide sequence that hybridizes under stringent conditions to the complement of SEQ ID NO:3, wherein said sequence encodes a polypeptide having LOX-like activity. And finally, claims 42-46 recite a nucleotide sequence comprising at least 50 contiguous nucleotide of SEQ ID NO:3 and encodes a polypeptide having LOX-like activity. Claims 37-46 therefore provide an additional functional/structural characteristic for the claimed sequences (*i.e.*, hybridization to the complement of the recited sequence or 50 contiguous nucleotides, where each sequence encodes a polypeptide having LOX-like activity). The necessary common features of the claimed genus are clear.

In summary, the description of a representative number of species *does not* require the description to be of such specificity that it would provide individual support for each species that the genus embraces. Applicants submit that the relevant identifying physical and chemical properties of the disclosed genus would be clearly recognized by one of skill in the art and consequently, Applicants were in possession of the necessary common attributes or features of the elements possessed by the members of the genus. Accordingly, the rejection of claims 2-4 under 35 U.S.C. §112, first paragraph, for lack of written description should be withdrawn and not applied to newly submitted claims 25-46.

Enablement

Claims 2-4 and 7 were rejected under 35 U.S.C. §112, first paragraph, for lack of enablement. Specifically, the Examiner has requested that a declaration under 37 C.F.R. 1.802

be provided. A Declaration in compliance with 37 C.F.R. 1.801-1.809 stating that the cDNA corresponding to SEQ ID NO:3 was deposited with the ATCC was previously submitted to the U.S. PTO on July 23, 2002. It is further noted that the deposit was made merely as a convenience to one of skill in the art and is not an admission that the deposit is required under 35 U.S.C. §112. And finally, the specification has been amended to provide the complete address of the depository. Applicants submit that the specification is now in compliance with 37 C.F.R. 1.809. The rejection of the claims with regard to the deposited sequence should be withdrawn.

Claims 2-4 and 7 were rejected under 35 U.S.C. §112, first paragraph, for lack of enablement. The Examiner asserts that the claims are not enabled as 1) the Applicant does not teach the enzymatic activity of the protein encoded by SEQ ID NO:3; 2) the Applicant does not teach the isolation of a nucleic acid molecule having 60% sequence identity to SEQ ID NO:3; and, 3) there is inherent unpredictability in the isolation of a nucleic acid sequence encoding a LOX enzyme. The Examiner concludes that the breath of the claims, unpredictability in the art, and lack of guidance would result in undue experimentation. The Applicants respectfully traverse, and submit claims 2-4 and 25-46 are fully enabled.

First, the Examiner acknowledges that the nucleic acid molecule of SEQ ID NO:3, a DNA construct comprising SEQ ID NO:3, and a transformed cell having a DNA construct comprising SEQ ID NO:3 are enabled. Newly submitted claims 27-36 are drawn to nucleic acid molecules, DNA constructs, cells, and vectors having a nucleic acid sequence comprising SEQ ID NO:3, a nucleotide sequence encoding SEQ ID NO:4, a corresponding antisense sequence, or a cDNA insert of the PTA-278 deposit. Applicants submit that claims 27-36 are enabled under 35 U.S.C. §112, first paragraph.

The Examiner further states that the "Applicant does not teach the isolation of nucleic acid molecules with 60% sequence identity to SEQ ID NO:3" and that the "Applicant does not teach the enzymatic activity of the protein encoded by SEQ ID NO:3" (Office Action mailed July 23, 2002, page 7). The Examiner is reminded that the specification need only describe the invention in such detail as to enable one of skill in the art to make and use it. Accordingly, the

Examiner's apparent suggestion that working examples are required to enable the instant invention is improper. As outlined in detail below, the specification provides both broad terminology and sufficient detail to enable the claims of the present invention.

Claims 2-4 have been amended to recite a sequence and related compositions "having at least 80% sequence identity" to the sequence of SEQ ID NO:3, wherein said sequence encodes a polypeptide having LOX-like activity. Claims 37-41 recite a sequence and related compositions comprising a nucleotide sequence that hybridizes under stringent conditions to the complement of SEQ ID NO:3 and encodes a polypeptide having LOX-like activity and claims 42-46 recite a sequence comprising at least 50 contiguous nucleotides of SEQ ID NO:3 and encoding a polypeptide having LOX-like activity. The specification enables the genus of sequences encompassed by these claims.

Applicant has provided the entire LOX-like amino acid sequence, SEQ ID NO:4, as well as a nucleotide sequence that encodes it, SEQ ID NO:3. The LOX-like nucleotide sequences of claims 2-4 and 25-46 vary from this sequence by specific structural parameters (*i.e.*, percent sequence identity to SEQ ID NO:3 (claims 2-4 and 25-26) or hybridization to the antisense of SEQ ID NO:3 (claims 37-41) or comprising fragments having at least 50 contiguous nucleotides of SEQ ID NO:3 (claims 42-46)). Guidance for determining percent sequence homology and hybridization conditions, and generating fragments are provided in the specification on pages 24-28, pages 20-23, and page 14, respectively.

Moreover, the nucleotide sequence of claims 2-4, 25-26, and 37-46 encode a polypeptide having "LOX -like activity" and therefore encompass functional variants. As described in the specification, "variant proteins encompassed by the present invention are biologically active, that is they possess the desired biological activity of the native protein" (page 15, lines 14-25). Guidance regarding alterations that allow the sequence to retain LOX-like activity is also provided. See, for example, pages 15 and 16, which provide guidance regarding conservative substitutions of amino acids.

And finally, the specification provides guidance regarding methods for assaying LOX-like activity. See, for example page 15, lines 14-25 that provides routine screening assays for

LOX-like activity (*i.e.*, measuring LOX enzymatic activity or, alternatively, measuring an alteration in the defense response). Accordingly, one of skill in the art would be able to determine the functionality of LOX-like polypeptides encompassed by the claimed invention.

Thus, a rational scheme for identifying sequences encompassed by the claims based on the guidance in the specification is provided and the skilled artisan could choose among possible modifications to produce nucleotide sequences within the parameters set forth in the claims and then test these modified variants to determine if they retain LOX-like activity. Although some quantity of experimentation would be required, the level of experimentation would not be undue in view of the amount of direction provided in the specification, the state of the prior art, and the level of skill of one of ordinary skill in the art.

The Federal Circuit has repeatedly stated that enablement is not precluded by the necessity for some experimentation, so long as the experimentation needed to practice the invention is not undue. *In re Wands*, 8 USPQ2d 1400 (Fed Cir 1988). Furthermore, a considerable amount of experimentation is permissible, if it is merely routine, or if the specification provides a reasonable amount of guidance in which the experimentation should proceed. *Id.*

Applicants stress that when evaluating the quantity of experimentation required, the court looks to the amount of experimentation required to practice a single embodiment of the invention, rather than the amount required to practice every embodiment of the invention. For example, in *Wands*, the claims at issue were drawn to immunoassay methods using any monoclonal antibody having a binding affinity for HbsAg of at least 10^{-9} M. The PTO had taken the position that the claim was not enabled as it would take undue experimentation to make the monoclonal antibodies required for the assay. The Federal Circuit reversed, and held that the claims were enabled, as the amount of experimentation required to isolate monoclonal antibodies and screen for those having the correct affinity was not undue. *Id.* Clearly, the Federal Circuit did not contemplate that every antibody useful in the methods of the claim must be identified. Rather, the court considered the amount of experimentation required to identify one or a few monoclonal antibodies having the required affinity.

In the instant case, the quantity of experimentation required to practice the invention of claims 2-4 and 25-46 amounts to two steps, generating a nucleotide sequence having at least 80% sequence identity to SEQ ID NO:3 or a nucleotide sequence that hybridizes to the complement of SEQ ID NO:3 or a fragment of SEQ ID NO:3 and assaying for functional activity. Such assays, while routine in the art, have further been presented in the specification.

Ample guidance is therefore provided to allow one of skill in the art to identify additional sequences encompassed by claims 2-4, 25-26, and 37-46. Consequently, contrary to the Examiner's conclusions, the quantity of experimentation necessary and the amount of guidance presented in the specification is sufficient to enable the claimed polynucleotides as set forth in claims 2-4 and 25-46. The rejection of the claims under 35 U.S.C. §112, first paragraph, should be withdrawn.

In rejecting claims 2-4 under 35 U.S.C. §112, first paragraph, for lack of enablement, the Examiner asserts that the isolation of nucleotide sequence encoding a polypeptide having LOX-like activity is unpredictable. The Examiner cites Broun *et al.* (1998) *Science 282*:131-133 in support of this statement. Broun *et al.* teach that as few as 4 amino acid substitutions can convert a desaturase to a hydroxylase and as few as 6 amino acids result in conversion of a hydroxylase to a desaturase. However, the substitution generated by Broun *et al.* are not conservative and occur at a location that is strictly conserved among the oleate desaturases from *Arabidopsis, Zea mays, Glycine max, R. communis*, and *Brassica napus*. See page 131, column 2, line 26-31. Consequently, Broun *et al.* teaches away from making amino acid substitutions that conserve function of the polypeptide.

In view of the state of the prior art, the level of skill possessed by one of ordinary skill in the art, the level of predictability in the art, and the amount of direction provided in the specification, the nucleic acid molecules of claim 2-4 and newly submitted claims 25-46 could be made and used by one of ordinary skill in the art without undue experimentation. The rejection of the claims under 35 U.S.C. §112, first paragraph, should be withdrawn and not applied to the newly submitted claims.

The Examiner further rejects claim 4 under 35 U.S.C. §112, first paragraph, for not being enabled for all cells *in vivo* including animal cells. This rejection is respectfully traversed. Claim 4 is drawn to a cell having stably incorporated the recited nucleotide sequence. In addition, newly submitted claims 26, 29, 31, 34, 36, 39, 41, 44 and 46 also recite the term "cell". The Examiner's attention is drawn to page 45 which explains that a variety of eukaryotic expression systems, such as yeast, insect cell lines, plants, and mammalian cells can be used to express the nucleotide sequence of interest. Moreover, expression vectors, along with routine methods to introduce nucleotide sequences into these various cell types is provided. See, for example, pages 44-46 of the specification. Introduction of nucleotide sequences into these various systems encompassed by the term "cell" is routine in the art and thus the claims are fully enabled by the specification. The Examiner is respectfully requested to withdraw the rejection of claim 4 under 35 U.S.C. §112, first paragraph, and not apply the rejection to the newly submitted claims.

Moreover, it is noted that the Examiner has failed to establish a *prima facie* showing of lack of enablement. "[T]he PTO has the burden of giving reasons supported by the record as a whole, why the specification is not enabling ..." *In re Angstadt*, 537 F.2d 489, 190 USPQ 214, 219 (C.C.P.A. 1976) (citing *In re Armbruster*, 512 F.2d 676, 185 USPQ 152 (C.C.P.A. 1975). If the Examiner continues to maintain the rejection, the Applicants respectfully request a further explanation of the Examiner's position.

The Rejection of the Claims Under 35 U.S.C. § 112, Second Paragraph, Should Be Withdrawn

Claims 2 and 4 were rejected under 35 U.S.C. §112, second paragraph, for indefiniteness. This rejection is respectfully traversed.

First claims 2 and 4 were rejected for the term "overlapping clones". Claims 2 and 4 have been amended and no longer recite the biological deposit referred to by "overlapping clones". The amendment to the claims obviates the rejection.

Claim 2 was further rejected for the term "corresponding". Claim 2 has been amended and no longer recites the term and the rejection has been obviated.

Claim 2 was further rejected for the term "stringent conditions". Claim 2 has been amended and no longer recites the term and the rejection has been obviated. Newly submitted claims 37-41 continue to recite the term "stringent conditions". The claims, however, further recite that these conditions comprises "hybridization in 50% formamide, 1 M NaCl, and 1% SDS at 37°C and a wash in 0.1x SSC at 60°C to 65°C." Support for this amendment can be found on page 21, lines 30-31 and page 22, lines 1-2 of the specification. Accordingly, newly submitted claims 37-41 satisfy the requirements of 35 U.S.C. §112, second paragraph.

Claim 2 was also rejected for the term "LOX-like" activity. This rejection is respectfully traversed. The Examiner asserts that it is unclear if the polypeptide has LOX activity or not. To determine the acceptability of claim language, one must determine if one of skill in the art would understand what is claimed, in view of the specification. The Examiners attention is drawn to page 15, lines 8-11 which provides various assays that can be used to measure LOX-like activity including, for example, assays to measure the defense response or enzymatic activity of LOX. When the term "LOX-like" is read in view of the specification, one of skill in the art would clearly understand the activity encompassed by the phrase "LOX-like". The requirements of 35 U.S.C. §112, second paragraph, have been satisfied.

Accordingly the rejection of the claims under 35 U.S.C. §112, second paragraph, should be withdrawn and not applied to the newly submitted claims.

The Rejection of the Claims Under 35 U.S.C. §102 Should Be Withdrawn

Claims 2-4 and 7 were rejected under 35 U.S.C. §102 as being anticipated by Rance *et al.* (1998) *PNAS* 95:6554-6559. This rejection is respectfully traversed.

The Examiner asserts that Rance *et al.* teaches a LOX gene, a promoter, and a transformed host cell and thus discloses all of the limitation of the claims. The Examiners comments regarding the relationship to the claimed sequences have been considered. However, the Examiner has provided nothing more than a mere assertion that the reference discloses sequences related to the claimed invention.

Claims 2-4 and 25-26 recite nucleotide sequences and related compositions having at least 80% sequence identity to SEQ ID NO:3; claims 37-41 recite nucleotide sequences and related compositions that hybridize under stringent conditions to SEQ ID NO:3; wherein the stringent conditions comprise "hybridization in 50% formamide, 1 M NaCl, and 1% SDS at 37°C and a wash in 0.1x SSC at 60°C to 65°C"; and, claims 42-46 recite sequences and related compositions having at least 50 contiguous nucleotides of SEQ ID NO:3. To the extent Applicant is able to understand the relationship of the claimed sequence to Rance *et al.*, Applicants believe newly submitted claims 2-4 and 25-46 are novel. If the rejection under 35 U.S.C. §102 in view of Rance *et al.* is maintained or applied to the newly submitted claims, the Examiner is respectfully requested to provide a Blast analysis which demonstrates the relationship of the claimed sequences to the those disclosed by Rance *et al.*

Consideration Of Previously Submitted Information Disclosure Statement

It is noted that an initialed copy of the PTO Form 1449 that was submitted with Applicants' Information Disclosure Statement filed April 25, 2001, September 27, 2001, and March 4, 2002 has not been returned to Applicants' representative with the Office Action. Accordingly, it is requested that an initialed copy of the Form 1449 be forwarded to the undersigned with the next communication from the PTO. In order to facilitate review of the references by the Examiner, a copy of the Information Disclosure Statement's 1449 Forms are attached hereto. Copies of the cited references were provided at the time of filling the original Information Disclosure Statements, and, therefore, no additional copies of the references are submitted herewith. Applicants will be pleased to provide additional copies of the references upon the Examiner's request if it proves difficult to locate the original references.

CONCLUSION

Accordingly, in view of the above remarks, it is submitted that this application is now ready for allowance. Early notice to this effect is solicited.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,

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I hereby certify that this paper is being facsimile transmitted to the Patent and Trademark Office at Fax No. 703-872-9306 on the date shown below. Pamela Lockley (Type or print name of person signing certification.) Pamela Lockley 10/23/02 Signature Date	I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, DC 20231, on October 23, 2002. _____

Version with Markings to Show Changes Made:

In the Specification

Please amend page 1, lines 1-2 of the specification as follows:

[SUNFLOWER RhoGAP,] LOX[, ADH AND SCIP-1]
POLYNUCLEOTIDES AND RELATED COMPOSITIONS [METHODS OF USE]

Please amend page 11, lines 27-31 and page 12, lines 1-12 of the specification as follows:

Plasmids containing the nucleotide sequences of the invention were deposited with the Patent Depository of the American Type Culture Collection (ATCC), 10801 University Drive, Manassas, Virginia, 20110-2209 and assigned Accession Nos. PTA-284, PTA-285, PTA-286, PTA-287, PTA-288, and PTA-559. Two of these plasmids, designated PHP15631 (Accession No. PTA-284) and PHP15632 (Accession No. PTA-285) contained overlapping clones. PHP15631 and PHP 15632 comprises the 5' and the 3' end of the rhoGAP sequence, respectively. It is noted, however, that clones PHP15631 and PHP15632 contain common sequences at the regions where they overlap. One of skill in the art by sequencing the clones and aligning the overlap may obtain the entire sequence of the sunflower rhoGAP. These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. These deposits were made merely as a convenience for those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112.

Please amend page 81 of the specification with the following:

[SUNFLOWER RhoGAP,] LOX[, ADH AND SCIP-1]
POLYNUCLEOTIDES AND RELATED COMPOSITIONS [METHODS OF USE]

ABSTRACT OF THE DISCLOSURE

Methods and compositions for modulating development and defense response are provided. Nucleotide sequences encoding a [sunflower rhoGAP,] LOX[, ADH, and SCIP-1] protein are provided. Nucleotide sequences comprising the LOX promoter are also provided. The sequences can be used in expression cassettes for modulating development, developmental pathways, and the plant defense response. Transformed plants, plant cells, tissues, and seed are also provided.

In the Claims

Please cancel claims 1, 5-24 without prejudice or disclaimer.

Please amend claim 2 as follows:

2. (Amended) An isolated nucleic acid molecule [selected from the group consisting of:

(a) a nucleic acid molecule comprising a nucleotide sequence set forth in SEQ ID NO: 1, 3, 6 or 8;

(b) a nucleic acid molecule comprising a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO: 2, 4, 7 or 9;

(c) a nucleic acid molecule comprising a nucleotide sequence deposited as Accession Nos. PTA-284, PTA-285, PTA-286, PTA-287, or PTA-288;

(d) a nucleic acid molecule comprising a nucleotide sequence obtained from the overlapping clones deposited as Accession No. PTA-284 and PTA-285;

(e) a nucleic acid molecule comprising an antisense sequence corresponding to a sequence of a), b), c), or d);

(f) a nucleic acid molecule comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequences of a), b), c), d), or e), wherein said sequence encodes a polypeptide having rhoGAP-, LOX-, SCIP-1, or ADH-like activity;

(g) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 1, wherein said sequence encodes a polypeptide having rhoGAP-like activity;

(h) a nucleic acid molecule] comprising a nucleotide sequence having at least [60%] 80% sequence identity to the sequence set forth in SEQ ID NO: 3, wherein said sequence encodes a polypeptide having LOX-like activity[;

(i) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 6, wherein said sequence encodes a polypeptide having ADH-like activity; and,

(j) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 8, wherein said sequence encodes a polypeptide having SCIP-1-like activity].

3. (Amended)A DNA construct comprising [a] the nucleotide sequence of claim 2, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a host cell.

4. (Amended) A cell having stably incorporated into its genome at least one DNA construct of claim 3 [comprising a nucleotide sequence operably linked to a promoter that drives expression in said cell, wherein said nucleotide sequence is selected from the group consisting of:

(a) a nucleic acid molecule comprising a nucleotide sequence set forth in SEQ ID NO: 1, 3, 6 or 8;

(b) a nucleic acid molecule comprising a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO: 2, 4, 7 or 9;

(c) a nucleic acid molecule comprising a nucleotide sequence deposited as Accession Nos. PTA-284, PTA-285, PTA-286, PTA-287, or PTA-288;

(d) a nucleic acid molecule comprising a nucleotide sequence obtained from the overlapping clones deposited as Accession No. PTA-284 and PTA-285;

(e) a nucleic acid molecule comprising an antisense sequence corresponding to a sequence of a), b), c), or d);

(f) a nucleic acid molecule comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequences of a), b), c), d), or e), wherein said sequence encodes a polypeptide having rhoGAP-, LOX-, SCIP-1, or ADH-like activity;

(g) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 1, wherein said sequence encodes a polypeptide having rhoGAP-like activity;

(h) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 3, wherein said sequence encodes a polypeptide having LOX-like activity;

(i) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 6, wherein said sequence encodes a polypeptide having ADH-like activity; and,

(j) a nucleic acid molecule comprising a nucleotide sequence having at least 60% sequence identity to the sequence set forth in SEQ ID NO: 8, wherein said sequence encodes a polypeptide having SCIP-1-like activity].